



SEQUENCE LISTING

<110> Bruce, Wesley B.

<120> A Nitrate-Responsive Root
Transcriptional Factor

<130> 1263

<140> US 09/970,624

<141> 2001-10-04

<150> US 60/238,292

<151> 2000-10-05

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1280

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (360)...(1082)

<400> 1

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catcattccc	ctctcgcgcta	gcttcttctt	ctctctctcc	cctcctctcc	ttcctcttcc	120
tcctcccttg	ggaaacctgc	tgccctttgag	ctttcttctt	cgagagctcc	caccagatct	180
cctctctctt	accttctttg	gcacgttcgg	cggcgcgcgc	ggagaaagat	agatccccgc	240
atcgctcgct	tcggtccttg	cttccgatcg	gagggccaca	accacaacct	ctcgtcccat	300
agcgtgcaag	cgcgagccag	ggtcaagaag	agagctagct	agctataggc	cggagatcg	359
atg ggg agg	gga aag atc	gtg atc	cgc agg atc	gat aac tcc	acg agc	407
Met Gly Arg	Gly Lys Ile	Val Ile Arg	Arg Ile Asp	Asn Ser Thr	Ser	15
1	5	10	15	20	25	
cgg cag gtg	acc ttc tcc	aag cgc cgg	aac ggg atc	ttc aag aag	gcc	455
Arg Gln Val	Thr Phe Ser	Lys Arg Arg	Asn Gly Ile	Phe Lys Ala		30
	20	25				
aag gag ctc	gcc atc ctc	tcg gat gcg	gag gtc ggc	ctc gtc atc	ttc	503
Lys Glu Leu	Ala Ile Leu	Cys Asp Ala	Glu Val Gly	Leu Val Ile	Phe	45
	35	40				
tcc agc acc	ggc cgc ctc	tac gag tac	tct agc acc	agc atg aaa	tca	551
Ser Ser Thr	Gly Arg Leu	Tyr Glu Tyr	Ser Ser Thr	Ser Met Lys	Ser	60
	50	55				
gtt ata gat	cgg tac ggc	aag gcc aag	gaa gag cag	caa gtc gtc	gca	599
Val Ile Asp	Arg Tyr Gly	Lys Ala Lys	Glu Glu Gln	Gln Val Val	Ala	80
	65	70	75			
aat ccc aac	tcg gag ctt	aag ttt tgg	caa agg gag	gca gca agc	ttg	647
Asn Pro Asn	Ser Glu Leu	Lys Phe Trp	Gln Arg Glu	Ala Ala Ser	Leu	

aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga 695
 Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
 100 105

gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat 743
 Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
 115 120 125

caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc 791
 Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
 130 135 140

ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac 839
 Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
 145 150 155 160

caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa 887
 Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
 165 170 175

aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga 935
 Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
 180 185 190

gtt aat cgg gag tca cgg act cca ttc aac ttt gca gta gta gaa acc 983
 Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
 195 200 205

aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat 1031
 Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
 210 215 220

aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca 1079
 Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
 225 230 235 240

tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg 1132
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aagagatgat actcagagaa agacatatatt gtggcagggga gatttgagat atgaacttat 1192
 aaatgtaatg caaataattt tcagaccgga atggggctcgt ggaattcaga ggatgattgc 1252
 tttctaaaaa aaaaaaaaaa aaaaaaaaaa 1280

<210> 2

<211> 240

<212> PRT

<213> Zea mays

<400> 2

Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser
 1 5 10 15
 Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
 20 25 30
 Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe
 35 40 45

Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
 50 55 60
 Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
 65 70 75 80
 Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
 85 90 95
 Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
 100 105 110
 Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
 115 120 125
 Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
 130 135 140
 Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
 145 150 155 160
 Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
 165 170 175
 Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
 180 185 190
 Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
 195 200 205
 Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
 210 215 220
 Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
 225 230 235 240

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 <211> 36
 <212> DNA
 <213> Artificial Sequence

<400> 3
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36